Claims:

1. Tools for the diagnostics, molecular definition and therapy development for chronic inflammatory joint diseases and other inflammatory, infectious or tumorous diseases in the human, whereat these tools are realized under the employment of the sequences of single genes, a selection of genes or the entirety of the genes mentioned in table 1 and of the genes coding for the proteins mentioned in table 2.

2. Tools according to claim 1, characterized in that they include gene sequences, which in respect to their sequence are identical with the genes mentioned in table 1 or with the genes coding for the proteins mentioned in table 2, or which have a respective sequence identity of at least 80% in the protein-coding regions.

3. Tools according to claims 1 and 2, characterized in that they include sequence sections or partial sequences, which in respect to their sequence are identical with the genes mentioned in table 1 and the genes subsumed under claim 2, or which have a sequence identity of at least 80% with the respective sections of the mentioned genes.

4. Tools according to claims 1 to 3, characterized in that, they are based on the employment of a

4.1. High-Throughput method of (micro-) array-hybridisation

4.2. High-Throughput method using techniques of the polymerase chain reaction for (semi-) quantification.

5. Tools according to claims 1 to 3, characterized in that they are based on the employment of a labeled patient sample and a second, differently labeled control sample, which is used for a comparative double hybridisation to a (micro-) array together with the patient sample (comparative red/green hybridisation).

6. Tools according to claims 1 to 5 for diagnostic purposes, characterized in that they are based on the employment of single, a selection, or the entirety of proteins or peptides deduced from the gene sequences in claims 1 to 3.

7. Tools according to claim 6, characterized in that they are based on the employment of single proteins, a selection of proteins or the entirety of the proteins mentioned in table 2.

8. Tools according to claims 6 and 7, characterized in that they are based on the use of partial sequences of single proteins, a selection of proteins or the entirety of the proteins mentioned in table 1.

9. Tools according to claims 6 to 8, characterized in that they include proteins or partial protein sequences, which in respect to their sequence are identical with the proteins deduced in table 1 or with the proteins mentioned in table 2, or which have a respective sequence identity of at least 80%.

10. Tools according to claims 6 to 9, characterized in that they are based on the employment of

10.1. High-Throughput methods in the analytics of protein expression (high definition, two-dimensional protein gel electrophoresis, MALDI techniques)

10.2 High-Throughput methods in the protein spotting technique (protein arrays) designed to screen for auto-antibodies as diagnostic tools for inflammatory joint diseases and other inflammatory, infectious or tumorous diseases in the human

10.3 High-Throughput methods in the technique of protein spotting (protein arrays) designed to screen for autoreactive T cells as diagnostic tools for inflammatory joint diseases and other inflammatory, infectious or tumorous diseases in the human

10.4 Non-High-Throughput methods in the technique of protein spotting designed to screen for autoreactive T cells as diagnostic tools for inflammatory joint diseases and other inflammatory, infectious or tumorous diseases in the human.

11. Tools according to claims 6 to 9, characterized in that they are based on the employment of antibodies, which are specific for proteins or partial sequences specified in claims 6 to 9.

12. Tools according to claims 1 to 11, characterized in that they are based on the use of the corresponding homologous sequences of another species for the analytics in animal experiments or for the diagnostics in animals with inflammatory joint diseases and other inflammatory, infectious or tumorous diseases.

13. Tools according to claims 6 to 11 as diagnostic tools for the detection of genetic alterations (mutations) in the genes mentioned in claims 1 to 3 or in the regulatory sequences (promoter, enhancer, silencer, specific sequences for binding further regulatory factors) of theses genes.

14. Tools according to claims 6 to 11 and 13 for the detection of genetic alterations (mutations) in the genes coding for the proteins mentioned in table 2 or in the regulatory sequences (promoter, enhancer, silencer, specific sequences for binding further regulatory factors) of these genes.

15. Tools according to claims 1 to 5 for the molecular definition of inflammatory joint diseases and other inflammatory, infectious or tumorous diseases in the human, whereat these tools are realized under the employment of the genes or DNA-sequences mentioned in the claims 1-3 or the respective, deduced proteins or peptides and of the proteins and partial protein sequences from claims 6 to 9 or their corresponding, coding gene sequences.

16. Tools according to claims 1 to 5 for the selection of a therapy for inflammatory joint diseases and other inflammatory, infectious or tumorous diseases in the human, whereat these tools employ the genes or DNA-sequences mentioned in claims 1-3 or the respective, deduced proteins or peptides.

17. Tools according to claims 1 to 5 for monitoring the progression/controlling the therapy of inflammatory joint diseases and other inflammatory, infectious or tumorous diseases in the human, whereat these tools employ the genes or DNA-sequences mentioned in claims 1-3 or the respective, deduced proteins or peptides.

18. Tools according to claims 1 to 5 as molecular tools for the development of therapy concepts, which include the direct or indirect impact on the expression of the genes or gene sequences mentioned in claims 1-3.

19. Tools according to claims 1 to 5 and 18 for the development of therapy concepts, which include the direct or indirect impact on the expression of the proteins or partial protein sequences mentioned in claims 6 to 9.

20. Tools according to claims 1 to 5 and 18 to 19 for the development of therapy concepts, which include the direct or indirect impact on the autoreactive T cells being directed against the proteins or partial protein sequences mentioned in claims 8-11.

21. Tools according to claims 1 to 5 and 18 to 20 for affecting the biological action of the proteins deduced from the gene sequences mentioned in claims 1 to 3.

22. Tools according to claims 1 to 5 and 18 to 21 for affecting the direct molecular regulatory circuits/pathways, in which the genes mentioned in claims 1-3 and the respective, deduced proteins, are involved.

23. Tools according to claims 1 to 5 and 18 to 22 for developing therapy concepts under the design and employment of interpretation algorithms using the mentioned genes and sequences and their regulatory mechanisms, in order to recognize or predict therapy concepts, therapy effects, therapy optimizations or diseases prognoses.

24. Tools according to claims 1 to 5 and 18 to 22 for developing biologically active drugs (Biologicals) under the employment of genes, gene sequences, the regulation of genes or gene sequences, or under the employment of proteins, protein sequences, fusion proteins according to claims 1 to 3 and 6 to 9 or under the employment of antibodies or autoreactive T cells according to claims 10 to 14.

25. Array as a molecular tools, being comprised of different antibodies or molecules with a comparable protein-specific binding behaviour, which are intended for the detection of the entirety of or a selection of the proteins deduced from the genes in table 1 or for the detection of the entirety of or a selection of the proteins in table 2.

26. Employment of tools according to claims 1 to 24 for the

26.1. Analysis of blood samples or tissue samples in medical diagnostics

26.2. Use in analytics according to example 1

26.3. Use in therapy concepts according to example 2.